



## RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/505,474  
Source: PCR/1P  
Date Processed by STIC: 8/31/04

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 06/05/04):  
U.S. Patent and Trademark Office, 220 20<sup>th</sup> Street S., Customer Window, Mail Stop Sequence, Crystal Plaza Two, Lobby, Room 1B03, Arlington, VA 22202

## Raw Sequence Listing Error Summary

### ERROR DETECTED

### SUGGESTED CORRECTION

SERIAL NUMBER: 10/505,474

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ **Wrapped Nucleics  
Wrapped Aminos** The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
  
- 2 ☐ **Invalid Line Length** The rules require that a line not exceed 72 characters in length. This includes white spaces.
  
- 3 ☒ **Misaligned Amino  
Numbering** The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
  
- 4 ☒ **Non-ASCII** The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
  
- 5 ☐ **Variable Length** Sequence(s) \_\_\_\_\_ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
  
- 6 ☐ **PatentIn 2.0  
"bug"** A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) \_\_\_\_\_. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
  
- 7 ☐ **Skipped Sequences  
(OLD RULES)** Sequence(s) \_\_\_\_\_ missing. If intentional, please insert the following lines for each skipped sequence:  
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
 This sequence is intentionally skipped  
  
 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
  
- 8 ☐ **Skipped Sequences  
(NEW RULES)** Sequence(s) \_\_\_\_\_ missing. If intentional, please insert the following lines for each skipped sequence.  
 <210> sequence id number  
 <400> sequence id number  
 000
  
- 9 ☐ **Use of n's or Xaa's  
(NEW RULES)** Use of n's and/or Xaa's have been detected in the Sequence Listing.  
 Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
  
- 10 ☐ **Invalid <213>  
Response** Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
  
- 11 ☐ **Use of <220>** Sequence(s) \_\_\_\_\_ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
  
- 12 ☐ **PatentIn 2.0  
"bug"** Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
  
- 13 ☐ **Misuse of n/Xaa** "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid



PCT

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/505,474

DATE: 08/31/2004  
TIME: 16:32:27

Input Set : A:\PTO.FG.txt  
Output Set: N:\CRF4\08312004\J505474.raw

3 <110> APPLICANT: OJI PAPER CO., LTD.  
5 <120> TITLE OF INVENTION: Cellulolytic enzyme and use thereof  
7 <130> FILE REFERENCE: PH-1724-PCT  
C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/505,474  
C--> 9 <141> CURRENT FILING DATE: 2004-08-24  
9 <160> NUMBER OF SEQ ID NOS: 52  
11 <170> SOFTWARE: PatentIn Ver. 3.1

*IMPORTANT!*  
*see item 4*  
*on Ena*  
*summary*  
*sheet*

*pp 1-5, 8, 9*

**Does Not Comply**  
**Corrected Diskette Needed**

## ERRORED SEQUENCES

450 <210> SEQ ID NO: 5  
451 <211> LENGTH: (28) 19 shown below  
452 <212> TYPE: DNA  
453 <213> ORGANISM: Artificial Sequence  
455 <220> FEATURE:  
456 <223> OTHER INFORMATION: Synthetic DNA  
458 <400> SEQUENCE: 5  
E--> 459 taygaraaya avatthttt needs explanation in (2207-2237) section. See p. 8. 19  
462 <210> SEQ ID NO: 6  
463 <211> LENGTH: (19) 20 shown  
464 <212> TYPE: DNA  
465 <213> ORGANISM: Artificial Sequence  
467 <220> FEATURE:  
468 <223> OTHER INFORMATION: Synthetic DNA  
470 <400> SEQUENCE: 6  
E--> 471 gayatcaagt tyatcratgg 20  
507 <210> SEQ ID NO: 8  
508 <211> LENGTH: 456  
509 <212> TYPE: PRT  
510 <213> ORGANISM: Coriolus hirsutus P.2  
512 <400> SEQUENCE: 8  
513 Met Phe Pro Thr Val Ser Leu Leu Ala Phe Ser Leu Leu Ala Thr Val  
514 1 5 10 15  
516 Tyr Gly Gln Gln Val Gly Thr Leu Thr Ala Glu Asn His Pro Arg Leu  
517 20 25 30  
519 Thr Val Gln Gln Cys Thr Ala Lys Asn Asn Cys Gln Thr Gln Gln His  
520 35 40 45  
522 Ser Val Val Leu Asp Ser Asn Trp Arg Trp Leu His Ala Thr Thr Gly  
523 50 55 60  
525 Ser Asn Asn Cys Tyr Thr Gly Asn Thr Trp Asp Ala Leu Leu Cys Pro  
526 65 70 75 80  
528 Asp Ala Thr Thr Cys Ala Lys Asn Cys Ala Val Asp Gly Ala Asp Tyr

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/505,474

DATE: 08/31/2004

TIME: 16:32:27

Input Set : A:\PTO.FG.txt

Output Set: N:\CRF4\08312004\J505474.raw

```

529          85          90          95
531 Ala Gly Thr Tyr Gly Ile Thr Thr Asn Gly Asn Ala Leu Thr Leu Lys
532          100          105          110
534 Phe Val Gln Gln Gly Pro Tyr Ser Lys Asn Ile Gly Ser Arg Val Tyr
535          115          120          125
537 Leu Met Asp Ala Gln Asp Gln Lys Tyr Glu Leu Phe Asn Leu Lys Asn
538          130          135          140
540 Gln Glu Phe Thr Phe Asp Val Asp Met Ser Asn Leu Pro Cys Gly Leu
541 145          150          155          160
543 Asn Gly Ala Leu Tyr Phe Val Glu Met Asp Ala Asp Gly Gly Ala Ser
544          165          170          175
546 Arg Phe Pro Thr Asn Lys Ala Gly Ala Lys Tyr Gly Thr Gly Tyr Cys
547          180          185          190
549 Asp Thr Gln Cys Pro Gln Asp Ile Lys Phe Ile Asn Gly Val Ala Asn
550          195          200          205
552 Leu Glu Gly Trp Ala Gly Ser Pro Ser Asp Pro Asn Ser Gly Thr Gly
553          210          215          220
555 Ser Phe Gly Thr Cys Cys Asn Glu Met Asp Val Trp Glu Ala Asn Lys
556 225          230          235          240
558 Asn Gly Ala Ala Phe Thr Pro His Val Cys Ser Val Thr Ser Gln Thr
559          245          250          255
561 Arg Cys Glu Gly Thr Gln Cys Gly Asp Gly Asp Glu Arg Tyr Asp Gly
562          260          265          270
E--> 564 Leu Cys Asp Lys Asp Gly Cys Asp Phe Asn Ser Phe Arg Kaa Gly Asp
565          275          280          285
567 Gln Thr Phe Leu Gly Pro Gly Lys Thr Val Asp Thr Asn Ala Lys Phe
568          290          295          300
570 Thr Val Val Thr Gln Phe Leu Thr Asn Asn Asn Gln Thr Ser Gly Gln
571 305          310          315          320
573 Leu Ser Glu Ile Arg Arg Leu Tyr Val Gln Asn Gly Arg Val Ile Ala
574          325          330          335
576 Asn Ser Lys Thr Asn Val Pro Gly Leu Gly Ala Phe Asp Ser Ile Thr
577          340          345          350
579 Asp Gln Phe Cys Asn Ala Gln Lys Gln Val Phe Gly Asp Asp Asn Thr
580          355          360          365
582 Phe Glu Lys Leu Gly Gly Leu Asn Thr Met Gly Gln Ala Phe Gln Arg
583          370          375          380
585 Gly Met Ala Leu Val Met Ser Ile Trp Asp Asp His Ala Ala Gly Met
586 385          390          395          400
588 Leu Trp Leu Asp Ala Asp Tyr Pro Pro Thr Arg Pro Arg Pro Thr Pro
589          405          410          415
591 Val Val Ser Arg Gly Pro Cys Ser Ala Thr Ser Gly Asp Pro Ala Thr
592          420          425          430
594 Ile Glu Asn Ser Glu Ala Ser Ser Ser Val Thr Phe Ser Asn Ile Lys
595          435          440          445
597 Val Gly Pro Ile Gly Ser Thr Phe
598          450          455
855 <210> SEQ ID NO: 13
856 <211> LENGTH: 21

```

needs explanation  
in 22207-22237  
section. see  
p. 8.

P. 3

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/505,474

DATE: 08/31/2004

TIME: 16:32:27

Input Set : A:\PTO.FG.txt

Output Set: N:\CRF4\08312004\J505474.raw

857 <212> TYPE: DNA  
 858 <213> ORGANISM: Artificial Sequence  
 860 <220> FEATURE:  
 861 <223> OTHER INFORMATION: Synthetic DNA  
 863 <400> SEQUENCE: 13  
 E--> 864 cagtggggg actggtgcaa c  
 1022 <210> SEQ ID NO: 18  
 1023 <211> LENGTH: 1327  
 E--> 1024 <212> TYPE: CDNA invalid. Use DNA. Explain modification  
 1025 <213> ORGANISM: Coriolus hirsutus  
 1027 <400> SEQUENCE: 18  
 1029 aagcactcta ttgacaccgt catgttctcg tctaccctct ccttcgcgcg cctcgcgcgc 60  
 1030 gcgctcgtcg cgcccaactgc cgtcaacgct cacggtttca ttcatagaata tgagatcggc 120  
 1031 ggcaagagct actccggttg gctcccgttc tcggaccctt acgagagccc tgtcccgcgc 180  
 1032 cgcacgcgagc gcaagatccc gagtgacggc cctatccttg atgtcacttc tctgacatt 240  
 1033 gcctgcaaca agggggggcga gtctggcgctc aaggccatcg ccaactgcgc agcaggcgc 300  
 1034 cagatcacct ttgactggaa cagttggccc gcagatcaca tgggcccggg gaccacatac 360  
 1035 atggcgctctt gcaacgggtga ttgcgcgtct ttcgatgcct ccaacgcgaa gtggttcaag 420  
 1036 attgacgctg ccggctactc gaacggcaag tgggctgcca ccaagctcat tgagaacggc 480  
 1037 gccaaagtga ccagcaccat tccagcgcgc ctcaaggctg gtgaataact ggtcgcgtcat 540  
 1038 gagatcattg ctctccacga cgccgggtgcg cctcagttct accccagctg cgctcagggtg 600  
 1039 aaggtcactg gtggtggtag ccagggttccc tctggttctt ccctcgtgtc cattccgggg 660  
 1040 ctctacacca ttcaggagtt ccgcacatct ggtccgacag cttcaagagc tttgccattc 720  
 1041 ctggaccgcg ggtgcgcttc agtggctcca acagcggctc tggcgattct cagcctgctg 780  
 1042 cctcctctct taccacgcc gctacttctt cggcggcctc ccagtctgcg tctcgcgcgc 840  
 1043 aggttcacac ctccgcggag acctccgcgc aggcctcggc gacgtctgtt gcgtcccacg 900  
 1044 catcttccgc tgcacacact tctcggccg catccgcgtc gaagccctcg tcgacgggga 960  
 1045 ccggaagggtg ctctcttaag cgcactcgcc gcggcatggt caagcgcaac gtctctcacc 1020  
 1046 acgccaagcg ccaccaccat tgatttctct ttcttctctg cgctcttggtc tgtctcgaga 1080  
 1047 tctcgatatg cttcagagaa gcaactggtcg acgggatctc aatcgatgtt gatacagatg 1140  
 1048 ggttgactcc cctccgcgct ctgctccac cgcccgggg atagagtctt cgcgcgcgc 1200  
 1049 ttcttaacg ttattcattc ctgcctccgc ataagtctcc gcattgctat tatcggtgct 1260  
 1050 gctagccgcg acgactgccc gacgattgta ccggaataca acgcgcttg tctttgtga 1320  
 1051 aaaaaaa 1327  
 1154 <210> SEQ ID NO: 21  
 1155 <211> LENGTH: 216  
 1156 <212> TYPE: PRT  
 1157 <213> ORGANISM: Coriolus hirsutus  
 1159 <400> SEQUENCE: 21  
 1160 Ala Gly Pro Tyr Ser Leu Leu Leu Asp Gln Trp Gly Lys Asp Gly Ala  
 E--> 1161 1 2 5 5 10 10 15 15  
 1162 Thr Ser Gly Ser Gln Cys Ala Asn Leu Ile Ser Leu Ser Gly Ser Thr  
 1163 20 25 30  
 1164 Val Ala Trp Lys Thr Thr Trp Gln Trp Thr Gly Gly Ser Gly Val Lys  
 1165 35 40 45  
 1166 Ser Phe Thr Asn Ile Gln Leu Asn Glu Gly Leu Asn Lys Gln Leu Ser  
 1167 50 55 60  
 1168 Ala Ile Lys Ser Ile Pro Thr Thr Trp Gln Trp Ser Gln Ser Ala Ser  
 1169 65 70 75 80

see p. 4

Use "n" instead, and explain in <2207-2237 section.  
 misaligned amino acid numbers. See item 3 on Error Summary Sheet.

## RAW SEQUENCE LISTING

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Input Set : A:\PTO.FG.txt

Output Set: N:\CRF4\08312004\J505474.raw

1170 Gly Ser Ile Val Ala Asp Val Ala Tyr Asp Leu Phe Thr Ala Asn Thr  
 1171 85 90 95  
 1172 Ala Gly Gly Ser Asn Val Asn Glu Ile Met Ile Trp Leu Ala Asn Phe  
 1173 100 105 110  
 1174 Asn Ala Gly Pro Ile Ser Phe Gln Tyr Gly Ala Asp Gly Lys Pro Val  
 1175 115 120 125  
 1176 Pro Val Ala Ser Asn Leu Ser Leu Ala Gly His Thr Trp Asn Leu Tyr  
 1177 130 135 140  
 1178 Ser Gly Ser Asn Gly Ala Asn Ala Val Phe Ser Phe Leu Pro Thr Ser  
 1179 145 150 155 160  
 1180 Gly Thr Ile Thr Ser Phe Ser Gly Asp Val Asn Val Phe Leu Gln Tyr  
 1181 165 170 175  
 1182 Leu Thr Gln His Gln Gly Val Ser Thr Ser Gln Phe Leu Val Thr Ala  
 1183 180 185 190  
 1184 Gln Ala Gly Thr Glu Pro Thr Ser Gly Ser Ala Thr Leu Thr Thr Ser  
 1185 195 200 205  
 E--> 1186 Ala Tyr Ser Leu Ala Ile Asn **Xaa** *needs explanation. see p. 8*  
 1187 210 215  
 1214 <210> SEQ ID NO: 24  
 1215 <211> LENGTH: **(1889)** *1989 (p.5)*  
 1216 <212> TYPE: DNA  
 1217 <213> ORGANISM: Phanerochaete chrysosporium  
 1219 <400> SEQUENCE: 24  
 1220 atgaagtact tcttgcctc agtagcagcg acgcttgccc ttagtgcacc tgcgcttggt 60  
 1221 gtcgctgtct ggggccaatg cgggtgaagc atatgtgttc atatgagagg cgtacgagaa 120  
 1222 ggttgaccgc gcaacaggga atcggcttta gtgggagtag tacttgcat gctggcaatc 180  
 1223 actgcgttta tctgaacgat tgtgaggtca atgtcatttc aatgccatga tttgctgacc 240  
 1224 gatataccttg cagattattc gcaatgccag cccggcgcg cgacgaccac ggtccggctg 300  
 1225 acaagtacca ttgcttcaac gacatctacc gcaccatcaa gcagcaatag cctttgctcc 360  
 1226 ggcagccgca cgaagttcaa gtttttcggt gtcaatgagt ctggtgctga gttcggtaat 420  
 1227 ctcaacatcc cagggtgtct aggcacggac tacacctggc cttcgccgtc cagcatcgac 480  
 1228 gtaagtata catcatatca gagctgctaa gcagggttgc gatagtgat cactagttct 540  
 1229 tcatgggcaa gggattcaac accttcgcga ttccgttct catggagcgt atgagccctc 600  
 1230 ccgcgacggg cctcaccggt ccgtttgatc agacctatct gagcggctct cagacgggtac 660  
 1231 gccaaacgta atagctggac cttgcgggga gtaaggctga ccatcacctt acggcagatt 720  
 1232 gtcagctata tcaccggaaa ggggggctat gcgctcgtag accgtgagt acggctcgca 780  
 1233 cgcaagtagt aggaggtcat ctgatagtga aggactgcag cgcacaactt tatgatctac 840  
 1234 aatggcaca ccattagcga cacaacgcg tgagcactcc tttagtttcg tctctgcgtt 900  
 1235 agctccgttc tgatgataca acaacacagc ttccagactt gtacgtgtgc tctgcctgaa 960  
 1236 cccgcttggc cgttgatcat catagtgat cgttctcaca ggggtggcaca acctcgccac 1020  
 1237 cgtcttcgta cgtctgtttc catgcgtgaa gcctgcaagg gtcgcccctg atcgggttta 1080  
 1238 tagaaatcca accccaatgt cgtctttggt gaatgagttc ggcgtgtgtg ctactcttag 1140  
 1239 caacgagctt acagcttggc agatgtcatg aacgagccgc acgacattcc cgcacagacg 1200  
 1240 gtcttcaacc tgggtgagttg cggccgagtt tggggacttc tgtcaaactc attcggcggt 1260  
 1241 gtttccccct agaaccaagc cgctatcaac ggaatccgtg ctgcgggtgc cacctcgcaa 1320  
 1242 cttatccttg ttgagggcac tagctacact ggcgcctgga gtgagatcag accttcaca 1380  
 1243 cccgcagAAC ctgcccattg attgattgtt tcgcagcgtg gacgacttct tccggtaatg 1440  
 1244 gtgctgtctt tgggtgctatc caagatccca acaacaatgt tgccatcggt gagtgcggga 1500  
 1245 agcgtaccgg tctgccaagt gctcacgggt aagcgtggga aagagatgca ccagtacctc 1560

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/505,474

DATE: 08/31/2004

TIME: 16:32:27

Input Set : A:\PTO.FG.txt

Output Set: N:\CRF4\08312004\J505474.raw

```

1246 gacagcgcacg gctccggcac gtcccccaca tgcgtttcgt ccacgatcgg tgcggagcgt 1620
1247 ctccaagcgg cgacacagtg gctgcagcag aacaacctga aaggcttcct gggtgagatc 1680
1248 ggagctgggtt cgaacgggtgc gtcggatcat gtctgtgtt gcagcctgtg ctgaccgtag 1740
1249 tcgttcaaac cagccgactg catcagtgcc gttcaggggtg cgctgtgcga gatgcaacag 1800
1250 tccggtgtct ggctcggcgc tctctggtgg gccgcaggcc catggtgggg cacggtacgt 1860
1251 gactgacctc ttgctgcgtg tgcacgtgca gactgctcat tgcgtccaca gtatttccaa 1920
1252 tcgatcgagc ccccgagtgg cgccgcgatc ccctccatcc tcccgcaggc actcgaaccc 1980

```

E--&gt; 1253 ttcctgtga

1989

1406 &lt;210&gt; SEQ ID NO: 29

1407 &lt;211&gt; LENGTH: 592 (592) 590(p.6)

1408 &lt;212&gt; TYPE: PRT

1409 &lt;213&gt; ORGANISM: Phanerochaete chrysosporium

1411 &lt;400&gt; SEQUENCE: 29

1413 Met Ile Pro Leu Arg Ser Ala Val Ala Ser Ser Leu Leu Leu Ala Ser

1414 1 5 10 15

1416 Leu Gly Ala Ala Gln Leu Pro Leu Pro Asn Pro Pro Trp Val Pro Leu

1417 20 25 30

1419 Asn Ala Thr Phe Gly Thr His Pro Ser Asn Pro Ser Asp Gly Ser Gly

1420 35 40 45

1422 Asn Pro His Trp Thr Asn Phe Leu Glu Asn Thr Leu Tyr Phe Tyr Glu

1423 50 55 60

1425 Glu Gln Arg Ser Gly Lys Leu Pro Val Thr Asn Arg Val Pro Trp Arg

1426 65 70 75 80

1428 Asn Asp Ser Ala Thr Asp Asp Gly Arg Asp Val Gly Leu Asp Leu Ser

1429 85 90 95

1431 Gly Gly Tyr Tyr Asp Ala Gly Asp Tyr Ile Lys Tyr Thr Phe Pro Met

1432 100 105 110

1434 Ser Phe Ser Val Met Ser Ile Cys Trp Gly Ala Leu Asp Tyr Gly Lys

1435 115 120 125

1437 Gly Tyr Asp Leu Ala Asn Gln Thr Ala Tyr Leu Asp Asp Met Leu Arg

1438 130 135 140

1440 Trp Ser Leu Asp Trp Leu Met Lys Ala His Pro Asp Pro Asn Thr Leu

1441 145 150 155 160

1443 Tyr Val Gln Val Gly Asp Ala Asp Leu Asp Asn Ala Tyr Trp Gly Gly

1444 165 170 175

1446 Asp Arg Gly Ile Pro Thr Pro Arg Thr Ser Tyr Ala Ile Asn Ser Thr

1447 180 185 190

1449 Ser Pro Gly Thr Asp Ala Ala Ala Gln Ala Ala Ala Ala Phe Ala Ala

1450 195 200 205

1452 Cys Ser Ala Leu Tyr Asn Asn Arg Thr Leu Ser Gln Pro Ala Pro Asn

1453 210 215 220

1455 Gly Ile Thr Ser Thr Ser Tyr Ala Ser Thr Leu Leu Gln His Ala Gln

1456 225 230 235 240

1458 Gln Leu Tyr Asn Phe Ala Thr Asn Ser Ser Val Pro Gln Val Thr Tyr

1459 245 250 255

1461 Gln Ala Ser Glu Pro Ser Val Ala Asp Ala Tyr Ala Ser Ser Gly Phe

1462 260 265 270

1464 Gln Asp Glu Leu Ala Ile Ala Ala Leu Phe Ile Ser Leu Ala Gly Asn

1465 275 280 285

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/505,474

DATE: 08/31/2004

TIME: 16:32:27

Input Set : A:\PTO.FG.txt

Output Set: N:\CRF4\08312004\J505474.raw

```

1467 Ser Ser Asp Ala Tyr Pro Gln Ala Ser Gln Val Tyr Arg Lys Gln Gly
1468      290                      295                      300
1470 Leu Ser Lys His Leu Glu Asp Asp Ala Val Phe Asn Trp Asp Glu Lys
1471 305                      310                      315                      320
1473 Ser Pro Gly Val Ala Leu Leu Ala Ala Gln Ile Ala Gln Lys Tyr Pro
1474      325                      330                      335
1476 Glu Leu Ala Asn Gly Thr Gly Val Asp Trp Lys Ser Asp Leu Asn Asn
1477      340                      345                      350
1479 Tyr Phe Asp Arg Ile Val Ser Asn Ser Gly Arg Ser Phe Leu Thr Ser
1480      355                      360                      365
1482 Gly Gly Leu Leu Tyr Tyr Pro Gly Asp Ser Asp Asp Ala Thr Leu Asn
1483      370                      375                      380
1485 Pro Ala Leu Asn Ala Ala Met Leu Leu Leu Arg Tyr Ala Asp Ser Gly
1486 385                      390                      395                      400
1488 Leu Ala Ser Ser Ser Glu Lys Gln Ser Ala Tyr Arg Gln Phe Ala Gln
1489      405                      410                      415
1491 Ser Gln Ile Asp Tyr Phe Leu Gly Asn Asn Pro Met Thr Val Gln Tyr
1492      420                      425                      430
1494 Met Val Gly Val His Pro Asn Ala Pro Ser Asn Pro His Ser Ala Leu
1495      435                      440                      445
1497 Ala Thr Gly Ala Thr Pro Gln Asp Ile Ala Asn Ile Asp Thr Val Pro
1498      450                      455                      460
1500 Glu His Glu Ala Tyr Val Leu Tyr Gly Gly Val Val Gly Gly Pro Asn
1501 465                      470                      475                      480
1503 Asp Asp Asp Leu Phe Trp Asp Leu Arg Ser Asp Trp Val Glu Ser Glu
1504      485                      490                      495
1506 Val Gly Leu Asp Tyr Val Ala Pro Val Val Thr Ile Ala Ala Arg Glu
1507      500                      505                      510
1509 Leu Val Ser Gly Ala Gly Asp Pro Trp Tyr Thr Gln Leu Gln Ala Gly
1510      515                      520                      525
1512 Ser Tyr Glu Glu Arg Arg Pro Gly Gly Gln Pro Cys Asp Ala Ala Ile
1513      530                      535                      540
1515 Ser Ala Gly Cys Arg Gly His Asp Trp Arg Val Gly Lys Ile Val Met
1516 545                      550                      555                      560
1518 Gly Ala Leu Val Gly Val Thr Gly Leu Val Val Leu Ser Leu Gly Thr
1519      565                      570                      575
1521 Val Trp Met Val Leu Ala Tyr Arg Asn Arg Ile Arg Lys Ile
E--> 1522      580                      585                      590
1788 <210> SEQ ID NO: 52
1789 <211> LENGTH: 24
1790 <212> TYPE: DNA
1791 <213> ORGANISM: Artificial
1793 <220> FEATURE:
1794 <223> OTHER INFORMATION: Synthetic DNA
1796 <400> SEQUENCE: 52
1797 ccattgggatg ttaggaatga tctg
E--> 1798

```

24

2/62  
delete



RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/10/505,474

DATE: 08/31/2004  
TIME: 16:32:28

Input Set : A:\PTO.FG.txt  
Output Set: N:\CRF4\08312004\J505474.raw

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,  
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:16,17,22,23,30,31,32,33,34,35,36,37,38,39,40,41,42,43,44,45,46,47,48,49

Seq#:50,51,52

## VARIABLE LOCATION SUMMARY

PATENT APPLICATION: US/10/505,474

DATE: 08/31/2004

TIME: 16:32:28

Input Set : A:\PTO.FG.txt

Output Set: N:\CRF4\08312004\J505474.raw

Use of n's or Xaa's (NEW RULES):

Use of n's and/or Xaa's have been detected in the Sequence Listing.

Use of &lt;220&gt; to &lt;223&gt; is MANDATORY if n's or Xaa's are present.

in &lt;220&gt; to &lt;223&gt; section, please explain location of n or Xaa, and which residue n or Xaa represents.

Seq#:5; N Pos. 19

Seq#:8; Xaa Pos. 286

Seq#:21; Xaa Pos. 216

10/505,474 9

<210> 1  
<211> 3420  
<212> DNA  
<213> Coriolus hirsutus

<220>

<223> Inventor: Akira, Tsukamoto; Seiji, Nakagame; Mari, Kabuto;  
Jun Sugiura; Hisako Sakaguchi; Atsushi Furujo

? does this  
have  
anything to  
do with  
Sequence I?

<223> response  
is used to  
describe  
particular  
details  
about that  
sequence.

Why not  
list the names  
under <1107>?

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/505,474

DATE: 08/31/2004

TIME: 16:32:28

Input Set : A:\PTO.FG.txt

Output Set: N:\CRF4\08312004\J505474.raw

L:9 M:270 C: Current Application Number differs, Replaced Current Application No  
L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:459 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:5  
L:459 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:5  
L:459 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0  
L:459 M:252 E: No. of Seq. differs, <211> LENGTH:Input:28 Found:19 SEQ:5 ✓  
L:471 M:252 E: No. of Seq. differs, <211> LENGTH:Input:19 Found:20 SEQ:6 ✓  
L:564 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:8 ✓  
L:864 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1 ✓  
L:1024 M:310 E: (3) Wrong or Missing Sequence Type, TYPE: ✓  
L:1161 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:21 ✓  
L:1186 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:21 ✓  
L:1253 M:252 E: No. of Seq. differs, <211> LENGTH:Input:1889 Found:1989 SEQ:24 ✓  
L:1522 M:252 E: No. of Seq. differs, <211> LENGTH:Input:592 Found:590 SEQ:29 ✓  
L:1798 M:254 E: No. of Bases conflict, LENGTH:Input:62 Counted:25 SEQ:52  
L:1798 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2 ✓  
L:1798 M:252 E: No. of Seq. differs, <211> LENGTH:Input:24 Found:25 SEQ:52 ✓